SEQUENCE LISTING

<110> GRAHAM, GARRY GEORGE
DONG, QIHAN

<120> METHOD OF INHIBITING PROSTATE CANCER CELL PROLIFERATION

<130> 47-216

<140> 10/517,256
<141> 2004-12-07

<150> PCT/AU03/00719
<151> 2003-06-10

<150> AU PS 2826
<151> 2002-06-07

<160> 9

<170> PatentIn Ver. 3.3

<210> 1
<211> 997
<212> DNA
<213> Homo sapiens

<400> 1
gaaggaaaaa gagcaacaga tccagggagc attcacctgc cctgtctcca aacagccttg 60
tgcctcacct acccccaacc tcccagaggg agcagctatt taaggggagc aggagtgcag 120
aacaaacaag acggcctggg gatacaactc tggagtcctc tgagagagcc accaaggagg 180
agcaggggag cgacggccgg ggcagaagtt gagaccaccc agcagaggag ctaggccagt 240
ccatctgcat ttgtcaccca agaactctta ccatgaagac cctcctactg ttggcagtga 300
tcatgatctt tggcctactg caggcccatg ggaatttggt gaatttccac agaatgatca 360
agttgacgac aggaaaggaa gccgcactca gttatggctt ctacggctgc cactgtggcg 420
tgggtggcag aggatccccc aaggatgcaa cggatcgctg ctgtgtcact catgactgtt 480
gctacaaacg tctggagaaa cgtggatgtg gcaccaaatt tctgagctac aagtttagca 540
actcggggag cagaatcacc tgtgcaaaac aggactcctg cagaagtcaa ctgtgtgagt 600
gtgataaggc tgctgccacc tgttttgcta gaaacaagac gacctacaat aaaaagtacc 660
agtactattc caataaacac tgcagaggga gcacccctcg ttgctgagtc ccctcttccc 720
tggaaacctt ccacccagtg ctgaatttcc ctctctcata ccctccctcc ctaccctaac 780
caagttcctt ggccatgcag aaagcatccc tcacccatcc tagaggccag gcaggagccc 840
ttctataccc acccagaatg agacatccag cagatttcca gccttctact gctctcctcc 900
acctcaactc cgtgcttaac caaagaagct gtactccggg gggtctcttc tgaataaagc 960
aattagcaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 997

<210> 2
<211> 2875
<212> DNA
<213> Homo sapiens

<400> 2
gaattctccg gagctgaaaa aggatcctga ctgaaagcta gaggcattga ggagcctgaa 60
gattctcagg ttttaaagac gctagagtgc caaagaagac tttgaagtgt gaaaacattt 120
cctgtaattg aaaccaaaat gtcatttata gatccttacc agcacattat agtggagcac 180
cagtattccc acaagtttac ggtagtggtg ttacgtgcca ccaaagtgac aaaggggccc 240
tttggtgaca tgcttgatac tccagatccc tatgtggaac tttttatctc tacaacccct 300

gacagcagga agagaacaag acatttcaat aatgacataa accctgtgtg gaatgagacc 360
tttgaattta ttttggatcc taatcaggaa aatgttttgg agattacgtt aatggatgcc 420
aattatgtca tggatgaaac tctagggaca gcaacattta ctgtatcttc tatgaaggtg 480
ggagaaaaga aagaagttcc ttttatttttc aaccaagtca ctgaaatggt tctagaaatg 540
tctcttgaag tttgctcatg cccagaccta cgatttagta tggctctgtg tgatcaggag 600
aagactttca gacaacagag aaaagaacac ataagggaga gcatgaagaa actcttgggt 660
ccaaagaata gtgaaggatt gcattctgca cgtgatgtgc ctgtggtagc catattgggt 720
tcaggtgggg gtttccgagc catggtggga ttctctggtg tgatgaaggc attatacgaa 780
tcaggaattc tggattgtgc tacctacgtt gctggtcttt ctggctccac ctggtatatg 840
tcaaccttgt attctcaccc tgattttcca gagaaagggc cagaggagat taatgaagaa 900
ctaatgaaaa atgttagcca caatcccctt ttacttctca caccacagaa agttaaaaga 960
tatgttgagt ctttatggaa gaagaaaagc tctggacaac ctgtcacctt tactgacatc 1020
tttgggatgt taataggaga aacactaatt cataatagaa tgaatactac tctgagcagt 1080
ttgaaggaaa aagttaatac tgcacaatgc cctttacctc ttttcacctg tcttcatgtc 1140
aaacctgacg tttcagagct gatgtttgca gattgggttg aatttagtcc atacgaaatt 1200
ggcatggcta aatatggtac ttttatggct cccgacttat ttggaagcaa atttttatg 1260
ggaacagtcg ttaagaagta tgaagaaaac cccttgcatt tcttaatggg tgtctggggc 1320
agtgcctttt ccatattgtt caacagagtt ttgggcgttt ctggttcaca aagcagaggc 1380
tccacaatgg aggaagaatt agaaaatatt accacaaagc atattgtgag taatgatagc 1440
tcggacagtg atgatgaatc acacgaaccc aaaggcactg aaaatgaaga tgctggaagt 1500
gactatcaaa gtgataatca agcaagttgg attcatcgta tgataatggc cttggtgagt 1560
gattcagctt tattcaatac cagagaagga cgtgctggga aggtacacaa cttcatgctg 1620
ggcttgaatc tcaatacatc ttatccactg tctcctttga gtgactttgc cacacaggac 1680
tcctttgatg atgatgaact ggatgcagct gtagcagatc ctgatgaatt tgagcgaata 1740
tatgagcctc tggatgtcaa aagtaaaaag attcatgtag tggacagtgg gctcacattt 1800
aacctgccgt atcccttgat actgagacct cagagagggg ttgatctcat aatctccttt 1860
gacttttctg caaggccaag tgactctagt cctccgttca aggaacttct acttgcagaa 1920
aagtgggcta aaatgaacaa gctccccttt ccaaagattg atccttatgt gtttgatcgg 1980
gaagggctga aggagtgcta tgtctttaaa cccaagaatc ctgatatgga gaaagattgc 2040
ccaaccatca tccactttgt tctggccaac atcaacttca gaaagtacaa ggctccaggt 2100
gttccaaggg aaactgagga agagaaagaa atcgctgact ttgatatttt tgatgaccca 2160
gaatcaccat tttcaacctt caattttcaa tatccaaatc aagcattcaa aagactacat 2220
gatcttatgc acttcaatac tctgaacaac attgatgtga taaaagaagc catggttgaa 2280
agcattgaat atagaagaca gaatccatct cgttgctctg tttcccttag taatgttgag 2340
gcaagaagat ttttcaacaa ggagtttcta agtaaaccca aagcatagtt catgtactgg 2400
aaatggcagc agtttctgat gctgaggcag tttgcaatcc catgacaact ggatttaaaa 2460
gtacagtaca gatagtcgta ctgatcatga gagactggct gatactcaaa gttgcagtta 2520
cttagctgca tgagaataat actattataa gttaggtgac aaatgatgtt gattatgtaa 2580
ggatatactt agctacattt tcagtcagta tgaacttcct gatacaaatg tagggatata 2640
tactgtattt ttaaacattt ctcaccaact ttcttatgtg tgttcttttt aaaaattttt 2700
tttcttttaa aatatttaac agttcaatct caataagacc tcgcattatg tatgaatgtt 2760
attcactgac tagatttatt cataccatga gacaacacta tttttattta tatatgcata 2820
tatatacata catgaaataa atacatcaat ataaaaataa aaaaaaacgg aattc 2875

<210> 3
<211> 144
<212> PRT
<213> Homo sapiens

<400> 3
Met Lys Thr Leu Leu Leu Leu Ala Val Ile Met Ile Phe Gly Leu Leu
1 5 10 15

Gln Ala His Gly Asn Leu Val Asn Phe His Arg Met Ile Lys Leu Thr
20 25 30

Thr Gly Lys Glu Ala Ala Leu Ser Tyr Gly Phe Tyr Gly Cys His Cys

```
         35                  40                  45

Gly Val Gly Gly Arg Gly Ser Pro Lys Asp Ala Thr Asp Arg Cys Cys
     50                  55                  60

Val Thr His Asp Cys Cys Tyr Lys Arg Leu Glu Lys Arg Gly Cys Gly
 65                  70                  75                  80

Thr Lys Phe Leu Ser Tyr Lys Phe Ser Asn Ser Gly Ser Arg Ile Thr
                 85                  90                  95

Cys Ala Lys Gln Asp Ser Cys Arg Ser Gln Leu Cys Glu Cys Asp Lys
            100                 105                 110

Ala Ala Ala Thr Cys Phe Ala Arg Asn Lys Thr Thr Tyr Asn Lys Lys
        115                 120                 125

Tyr Gln Tyr Tyr Ser Asn Lys His Cys Arg Gly Ser Thr Pro Arg Cys
    130                 135                 140


<210> 4
<211> 749
<212> PRT
<213> Homo sapiens

<400> 4
Met Ser Phe Ile Asp Pro Tyr Gln His Ile Ile Val Glu His Gln Tyr
  1               5                  10                  15

Ser His Lys Phe Thr Val Val Val Leu Arg Ala Thr Lys Val Thr Lys
             20                  25                  30

Gly Ala Phe Gly Asp Met Leu Asp Thr Pro Asp Pro Tyr Val Glu Leu
         35                  40                  45

Phe Ile Ser Thr Thr Pro Asp Ser Arg Lys Arg Thr Arg His Phe Asn
     50                  55                  60

Asn Asp Ile Asn Pro Val Trp Asn Glu Thr Phe Glu Phe Ile Leu Asp
 65                  70                  75                  80

Pro Asn Gln Glu Asn Val Leu Glu Ile Thr Leu Met Asp Ala Asn Tyr
                 85                  90                  95

Val Met Asp Glu Thr Leu Gly Thr Ala Thr Phe Thr Val Ser Ser Met
            100                 105                 110

Lys Val Gly Glu Lys Lys Glu Val Pro Phe Ile Phe Asn Gln Val Thr
        115                 120                 125

Glu Met Val Leu Glu Met Ser Leu Glu Val Cys Ser Cys Pro Asp Leu
    130                 135                 140

Arg Phe Ser Met Ala Leu Cys Asp Gln Glu Lys Thr Phe Arg Gln Gln
145                 150                 155                 160

Arg Lys Glu His Ile Arg Glu Ser Met Lys Lys Leu Leu Gly Pro Lys
```

```
                165                 170                 175

Asn Ser Glu Gly Leu His Ser Ala Arg Asp Val Pro Val Val Ala Ile
            180                 185                 190

Leu Gly Ser Gly Gly Gly Phe Arg Ala Met Val Gly Phe Ser Gly Val
        195                 200                 205

Met Lys Ala Leu Tyr Glu Ser Gly Ile Leu Asp Cys Ala Thr Tyr Val
    210                 215                 220

Ala Gly Leu Ser Gly Ser Thr Trp Tyr Met Ser Thr Leu Tyr Ser His
225                 230                 235                 240

Pro Asp Phe Pro Glu Lys Gly Pro Glu Glu Ile Asn Glu Glu Leu Met
                245                 250                 255

Lys Asn Val Ser His Asn Pro Leu Leu Leu Leu Thr Pro Gln Lys Val
            260                 265                 270

Lys Arg Tyr Val Glu Ser Leu Trp Lys Lys Lys Ser Ser Gly Gln Pro
        275                 280                 285

Val Thr Phe Thr Asp Ile Phe Gly Met Leu Ile Gly Glu Thr Leu Ile
    290                 295                 300

His Asn Arg Met Asn Thr Thr Leu Ser Ser Leu Lys Glu Lys Val Asn
305                 310                 315                 320

Thr Ala Gln Cys Pro Leu Pro Leu Phe Thr Cys Leu His Val Lys Pro
                325                 330                 335

Asp Val Ser Glu Leu Met Phe Ala Asp Trp Val Glu Phe Ser Pro Tyr
            340                 345                 350

Glu Ile Gly Met Ala Lys Tyr Gly Thr Phe Met Ala Pro Asp Leu Phe
        355                 360                 365

Gly Ser Lys Phe Phe Met Gly Thr Val Val Lys Lys Tyr Glu Glu Asn
    370                 375                 380

Pro Leu His Phe Leu Met Gly Val Trp Gly Ser Ala Phe Ser Ile Leu
385                 390                 395                 400

Phe Asn Arg Val Leu Gly Val Ser Gly Ser Gln Ser Arg Gly Ser Thr
                405                 410                 415

Met Glu Glu Glu Leu Glu Asn Ile Thr Thr Lys His Ile Val Ser Asn
            420                 425                 430

Asp Ser Ser Asp Ser Asp Asp Glu Ser His Glu Pro Lys Gly Thr Glu
        435                 440                 445

Asn Glu Asp Ala Gly Ser Asp Tyr Gln Ser Asp Asn Gln Ala Ser Trp
    450                 455                 460

Ile His Arg Met Ile Met Ala Leu Val Ser Asp Ser Ala Leu Phe Asn
465                 470                 475                 480
```

```
Thr Arg Glu Gly Arg Ala Gly Lys Val His Asn Phe Met Leu Gly Leu
                485                 490                 495

Asn Leu Asn Thr Ser Tyr Pro Leu Ser Pro Leu Ser Asp Phe Ala Thr
            500                 505                 510

Gln Asp Ser Phe Asp Asp Asp Glu Leu Asp Ala Ala Val Ala Asp Pro
        515                 520                 525

Asp Glu Phe Glu Arg Ile Tyr Glu Pro Leu Asp Val Lys Ser Lys Lys
    530                 535                 540

Ile His Val Val Asp Ser Gly Leu Thr Phe Asn Leu Pro Tyr Pro Leu
545                 550                 555                 560

Ile Leu Arg Pro Gln Arg Gly Val Asp Leu Ile Ile Ser Phe Asp Phe
                565                 570                 575

Ser Ala Arg Pro Ser Asp Ser Ser Pro Pro Phe Lys Glu Leu Leu Leu
            580                 585                 590

Ala Glu Lys Trp Ala Lys Met Asn Lys Leu Pro Phe Pro Lys Ile Asp
        595                 600                 605

Pro Tyr Val Phe Asp Arg Glu Gly Leu Lys Glu Cys Tyr Val Phe Lys
    610                 615                 620

Pro Lys Asn Pro Asp Met Glu Lys Asp Cys Pro Thr Ile Ile His Phe
625                 630                 635                 640

Val Leu Ala Asn Ile Asn Phe Arg Lys Tyr Lys Ala Pro Gly Val Pro
                645                 650                 655

Arg Glu Thr Glu Glu Glu Lys Glu Ile Ala Asp Phe Asp Ile Phe Asp
            660                 665                 670

Asp Pro Glu Ser Pro Phe Ser Thr Phe Asn Phe Gln Tyr Pro Asn Gln
        675                 680                 685

Ala Phe Lys Arg Leu His Asp Leu Met His Phe Asn Thr Leu Asn Asn
    690                 695                 700

Ile Asp Val Ile Lys Glu Ala Met Val Glu Ser Ile Glu Tyr Arg Arg
705                 710                 715                 720

Gln Asn Pro Ser Arg Cys Ser Val Ser Leu Ser Asn Val Glu Ala Arg
                725                 730                 735

Arg Phe Phe Asn Lys Glu Phe Leu Ser Lys Pro Lys Ala
            740                 745
```

<210> 5
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 5
Phe Leu Ser Tyr Lys
1 5

<210> 6
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 6
Phe Leu Ser Tyr Arg
1 5

<210> 7
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 7
tttgtcaccc aagaactctt ac 22

<210> 8
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 8
gggagggagg gtatgaga 18

<210> 9
<211> 18
<212> DNA
<213> Homo sapiens

<400> 9
gaggtaaatg gtattctc 18